

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:46:23 ; Search time 43.8955 Seconds

(without alignments)
1225.145 Million cell updates/sec

Title: US-09-988-971-2

Perfect score: 1351

Sequence: 1 MGSLEPSRRKSLPSLSVSSV.....RESLSFYISLNDVAVSLDDA 261

Scoring table: BLOSUM62

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:*

1: sp.archaea:*

2: sp.bacteria:*

3: sp.fungi:*

4: sp.human:*

5: sp.invertebrate:*

6: sp.mammal:*

7: sp.minc:*

8: sp.organelle:*

9: sp.phage:*

10: sp.plant:*

11: sp.rodent:*

12: sp.virus:*

13: sp.vertebrate:*

14: sp.unclassified:*

15: sp.virus:*

16: sp.bacteriap:*

17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1351	100.0	261	4 Q9H603	Q9H603 homo sapien
2	1040	77.0	197	4 Q9H135	Q9H135 homo sapien
3	1032	76.4	259	11 Q9V112	Q9V112 mus musculu
4	1023	75.7	259	11 Q9R410	Q9R410 mus musculu
5	938.5	69.5	210	4 Q8WY18	Q8WY18 homo sapien
6	751.5	55.6	179	11 Q9D129	Q9D129 mus musculu
7	495.5	36.7	280	11 Q8Q2X8	Q8Q2X8 mus musculu
8	495.5	36.7	281	11 Q6O898	Q6O898 mus musculu
9	485.5	35.9	276	4 Q13239	Q13239 homo sapien
10	370.5	27.4	502	13 Q9DDK6	Q9DDK6 salmo salar
11	365.5	27.1	488	13 Q13064	Q13064 xenopus lae
12	362.5	26.8	161	4 Q9HB17	Q9HB17 homo sapien
13	356.5	26.4	505	4 Q9G1N1	Q9G1N1 homo sapien
14	344	25.5	509	6 Q9SM32	Q9SM32 hylobates s
15	342.5	25.4	509	11 Q91X65	Q91X65 mus musculu
16	336	24.9	517	5 Q9V9J3	Q9V9J3 drosophila

17	332	24.6	509	6 Q95KR7	Q95KR7 salmifci sci
18	319.5	23.6	537	11 Q62844	Q62844 rattus norv
19	317.5	23.5	496	13 Q93411	Q93411 xenopus lae
20	313.5	23.2	541	11 Q99PM1	Q99PM1 rattus norv
21	313	23.0	812	15 Q85466	Q85466 y73 sarcoma
22	311	23.0	517	11 Q63206	Q63206 rattus norv
23	310	22.9	534	4 Q16248	Q16248 homo sapien
24	310	22.9	534	4 Q95M31	Q95M31 hylobates s
25	309	22.9	527	5 Q9Y121	Q9Y121 ephydatia f
26	308.5	22.6	517	5 Q77050	Q77050 antiochidari
27	306	22.6	63	4 Q96014	Q96014 homo sapien
28	292.5	21.7	587	15 Q64817	Q64817 avian sarco
29	289	21.4	511	5 Q8MCM5	Q8MCM5 strongyloce
30	288.5	21.4	503	5 Q8MCM5	Q8MCM5 ephydatia f
31	286	21.2	502	13 Q8G6J9	Q8G6J9 ligu rubrip
32	284.5	21.1	523	15 Q85477	Q85477 rous sarcom
33	284.5	21.1	526	15 Q64994	Q64994 rous sarcom
34	281.5	20.8	526	15 Q93080	Q93080 rous sarcom
35	280	20.7	535	15 Q92957	Q92957 rous sarcom
36	279.5	20.7	526	15 Q64993	Q64993 rous sarcom
37	279	20.7	546	15 Q63633	Q63633 rous sarcom
38	277.5	20.5	542	11 Q93J10	Q93J10 rattus norv
39	277.5	20.5	504	5 Q8WSU2	Q8WSU2 ephydatia f
40	277	20.5	545	15 Q86362	Q86362 rous sarcom
41	274.5	20.3	495	5 Q8WSU4	Q8WSU4 ephydatia f
42	274.5	20.2	526	15 Q07461	Q07461 rous sarcom
43	273.5	20.2	526	15 Q60567	Q60567 rous sarcom
44	272.5	20.2	507	5 Q45539	Q45539 caenorhabd
45	264.5	19.6	507	5 Q45539	Q45539 caenorhabd

ALIGNMENTS

RESULT 1	Q9H603	PRELIMINARY:	PRT:	261 AA.
ID	Q9H603			
AC	Q9H603			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DE	CDNA: F1221992.1 fs, clone HEP06554 (Src-like adaptor protein-2)			
DE	(Modulator of antigen receptor signaling MARS).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kawabata A., Hiki J. T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,			
RA	Okitani T., Nakamura Y., Isogai T., Sugano S.,			
RA	Tanaka T., Nakamura Y., Isogai T., Sugano S.,			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=21553259; PubMed=11696592;			
RA	Holland S.J., Liao X.C., Mendenhall M.K., Zhou X., Pardo J., Chu P.,			
RA	Spencer C., Fu A.C., Sheng N., Yu P., Pali E., Nagin A., Shen M.,			
RA	Yu S., Chan E., Wu X., Li C., Wolstschlaeger M., Aversa G.,			
RA	Kolbinger F., Bennett M.K., Molleaux S., Luo Y., Payan D.G.,			
RA	Mancebo H.S.Y., Wu J.,			
RT	"Functional cloning of src-like adapter protein-2 (SLAP-2), a novel			
RT	inhibitor of Antigen Receptor Signaling."			
RL	J. Exp. Med. 194:1263-1276(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=THYMUS;			
RA	Loreto M.P., McGlade C.J.,			
RA	"Modulator of Antigen Receptor Signaling (MARS)."			
RL	Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.			
DR	EMBL: AK025645; BAB15201.1; -.			

DR EMBL: AF326353; AAL29204.1; -
 DR EMBL: AF290985; AAL38197.1; -
 DR HSSP: P06239; ILKK.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRODOM: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR SH3 domain; Receptor.
 SO SEQUENCE 261 AA; 28585 MW; 858AF03451672B3D CRC64;

Query Match 100.0%; Score 1351; DB 4; Length 261;
 Best Local Similarity 100.0%; Pred. No. 2.2e-115;
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSLSRRKSLSPSSSSVGGPGPTMEAEKSKATVAALGSPAGAPALSLRGEPLT 60
 DB 1 MGSLSRRKSLSPSSSSVGGPGPTMEAEKSKATVAALGSPAGAPALSLRGEPLT 60
 QY 61 IVSEDDGMWTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPLPGNGAFLI 120
 DB 61 IVSEDDGMWTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPLPGNGAFLI 120
 QY 121 RESQTRRGGSYSLSVRLSRPASMDRIIRHRIHCLDNGMWLYISPRLTFFPSLOALVDHYSELA 180
 DB 121 RESQTRRGGSYSLSVRLSRPASMDRIIRHRIHCLDNGMWLYISPRLTFFPSLOALVDHYSELA 180
 QY 121 RESQTRRGGSYSLSVRLSRPASMDRIIRHRIHCLDNGMWLYISPRLTFFPSLOALVDHYSELA 180
 DB 121 RESQTRRGGSYSLSVRLSRPASMDRIIRHRIHCLDNGMWLYISPRLTFFPSLOALVDHYSELA 180
 QY 181 DDICCLLKEPCVQLQRAGPLPGKDIPLVYVQRTPLNWKELDSSLFSEATGESLSEGL 240
 DB 181 DDICCLLKEPCVQLQRAGPLPGKDIPLVYVQRTPLNWKELDSSLFSEATGESLSEGL 240
 QY 241 LRESLSFYISLNDENVSLDDA 261
 DB 241 LRESLSFYISLNDENVSLDDA 261

RESULT 2
 Q9H135 PRELIMINARY; PRT: 197 AA.
 AC Q9H135;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE D1977B1.1 (Novel protein tyrosine kinase with Src homology domain 2
 DE (SH2) domains) (Fragment).
 GN D1977B1.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lloyd D.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL050318; CAB75365.1; -
 DR HSSP: P06239; ILKK.
 DR InterPro: IPR000980; SH2.
 DR Pfam: PF00017; SH2; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRODOM: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR Kinase.
 FT NON_TER 1
 SO SEQUENCE 197 AA; 22124 MW; EF01FE7A85C5C1F1 CRC64;

Query Match 77.0%; Score 1040; DB 4; Length 197;
 Best Local Similarity 100.0%; Pred. No. 3.9e-87;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 65 DGDWMTVLSVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPLPGNGAFLIRESQ 124
 DB 1 DGDWMTVLSVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPLPGNGAFLIRESQ 60
 QY 125 TRRGYSLSVRLSRPASMDRIIRHRIHCLDNGMWLYISPRLTFFPSLOALVDHYSELA 184
 DB 61 TRRGYSLSVRLSRPASMDRIIRHRIHCLDNGMWLYISPRLTFFPSLOALVDHYSELA 120
 QY 185 CLLKEPCVQLQRAGPLPGKDIPLVYVQRTPLNWKELDSSLFSEATGESLSEGLRES 244
 DB 121 CLLKEPCVQLQRAGPLPGKDIPLVYVQRTPLNWKELDSSLFSEATGESLSEGLRES 180
 QY 245 LSFYISLNDENVSLDDA 261
 DB 181 LSFYISLNDENVSLDDA 197

RESULT 3
 Q8V142 PRELIMINARY; PRT: 259 AA.
 ID Q8V142;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Modulator of antigen receptor signaling MARS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Loreto M.P.; Meglade C.J.;
 RT Modulator of Antigen Receptor Signaling (MARS).
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF287467; AAL38196.1; -
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRODOM: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR Receptor.
 KM RECEPTOR.
 SO SEQUENCE 259 AA; 28476 MW; 8270F17CD3FC50A3 CRC64;

Query Match 76.4%; Score 1032; DB 11; Length 259;
 Best Local Similarity 79.8%; Pred. No. 3.1e-86;
 Matches 209; Conservative 16; Mismatches 33; Indels 4; Gaps 3;

QY 1 MGSLSRRKSLSPSSSSVGGPGPTMEAEKSKATVAALGSPAGAPALSLRGEPLT 60
 DB 1 MGSLSRRKSLSPSSSSVGGPGPTMEAEKSKATVAALGSPAGAPALSLRGEPLT 59
 QY 61 IVSEDDGMWTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPLPGNGAFLI 120
 DB 61 IVSEDDGMWTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPLPGNGAFLI 119
 QY 121 RESQTRRGGSYSLSVRLSRPASMDRIIRHRIHCLDNGMWLYISPRLTFFPSLOALVDHYSELA 180
 DB 121 RESQTRRGGSYSLSVRLSRPASMDRIIRHRIHCLDNGMWLYISPRLTFFPSLOALVDHYSELA 179
 QY 181 DDICCLLKEPCVQLQRAGPLPGKDIPLVYVQRTPLNWKELDSSLFSEATGESLSEGL 239
 DB 181 DDICCLLKEPCVQLQRAGPLPGKDIPLVYVQRTPLNWKELDSSLFSEATGESLSEGL 239
 QY 240 GLRESLSFYISLNDENVSLDDA 261
 DB 240 GLRESLSFYISLNDENVSLDDA 261

DB 240 GLRESLSYISLAE--PLDDA 259

RESULT 4

OB84LO PRELIMINARY; PRT: 259 AA.

AC 0844LO: 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Src-like adapter protein-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
 RA Pandey A., Ibarrol N., Kratchmarova I., Fernandez M.,
 RA Constantinescu S., Chava O., Sawasdikosol S., Lodish H.F., Mann M.;
 RT "A novel Src homology 2 domain-containing molecule, Src-Like Adapter
 RT Protein-2 (SLAP-2), which negatively regulates T cell receptor
 RT signaling";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN 121

RP SEQUENCE FROM N.A.
 RA Ibarrola N., Mann M., Pandey A.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF434990; AAL86403.1;
 SO SEQUENCE 259 AA; 28516 MW; 138868244152E34 CRC64;

Query Match 75.7%; Score 1023; DB 11; Length 259;
 Best Local Similarity 79.4%; Pred. No. 2.1e-85;
 Matches 208; Conservative 16; Mismatches 34; Indels 4; Gaps 3;

QY 1 MSLPSRRKSLSPSSLSVQGGPVYMEAEKSKATVALGSPAGPAELSLRLGPELT 60
 DB 1 MSLPSRRKSLSPSSLSVQGGPVYMEAEKSKATVALGSPAGPAELSLRLGPELT 59
 QY 61 IYSEDDMMWTVLSEVSGREYNIPSVHAKVSHGWLTCGLSREKAEELLLPGNGGAFIL 120
 DB 60 IYSEDDMMWTVLSEVSGREYNIPSVHAKVSHGWLTCGLSREKAEELLLPGNGGAFIL 119
 QY 121 RESQTRRGYSLSVRLSPASMDRIHRYHICLDNGWLYISPLTFPSLQALVDHYSELA 180
 DB 120 RESQTRRGYSLSVRLSPASMDRIHRYHICLDNGWLYISPLTFPSLQALVDHYSELA 179
 QY 181 DDICLLKEPCVLRAGPLPGKIDPLVYVORTPLNKKELDSLLFSEA-ATGESLISF 239
 DB 180 DDICLLKEPCVLRAGPLPGKIDPLVYVORTPLNKKELDSLLFSEA-ATGESLISF 239
 QY 240 GLRESLSYISLDAE--PLDDA 259
 DB 240 GLRESLSYISLDAE--PLDDA 259

RESULT 5

OB84LO PRELIMINARY; PRT: 210 AA.

AC 0844LO: 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 21, Last annotation update)
 DE Modulator of antigen receptor signaling, putative splice isoform
 DE MARS-V.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RC TISSUE=THYMUS;
 RA Loreto M.P., McGlade C.J.;
 RT "Modulator of Antigen Receptor Signaling (MARS) - putative splice

RT variant";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF290986; AAL8198.1;
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR01452; SH3.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR Prodom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Receptor.

SO SEQUENCE 210 AA; 23103 MW; BED62208E53A472E CRC64;

Query Match 69.5%; Score 938.5; DB 4; Length 210;
 Best Local Similarity 89.4%; Pred. No. 8.1e-78;
 Matches 185; Conservative 3; Mismatches 12; Indels 7; Gaps 1;

QY 1 MSLPSRRKSLSPSSLSVQGGPVYMEAEKSKATVALGSPAGPAELSLRLGPELT 60
 DB 1 MSLPSRRKSLSPSSLSVQGGPVYMEAEKSKATVALGSPAGPAELSLRLGPELT 60
 QY 61 IYSEDDMMWTVLSEVSGREYNIPSVHAKVSHGWLTCGLSREKAEELLLPGNGGAFIL 120
 DB 61 IYSEDDMMWTVLSEVSGREYNIPSVHAKVSHGWLTCGLSREKAEELLLPGNGGAFIL 120
 QY 121 RESQTRRGYSLSVRLSPASMDRIHRYHICLDNGWLYISPLTFPSLQALVDHYSE-- 178
 DB 121 RESQTRRGYSLSVRLSPASMDRIHRYHICLDNGWLYISPLTFPSLQALVDHYSE-- 180
 QY 179 -----LADICLLKEPCVLRAGPLP 200
 DB 181 PAVWGVTPTCDCAEDTTLERAGQLP 207

RESULT 6

OB84LO PRELIMINARY; PRT: 179 AA.

AC 09D129: 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE A30009E21Rik protein.
 GN A30009E21Rik.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=RETINA;
 RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schram L.M., Strandberg F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carlsberg P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;

Db 6 KSTSPSPSERPLSSS-----EGLESDFLAV-LMDYPSDISPIIFRGRKLVISDE 55
 QY 66 GDMVTVLSKREYNIPSVAVKSHGWLIGLSREKAEELLPLGNPGAFILRESQT 125
 Db 56 GGMKKAISLSTGRESYIPGICVAVYHGMWLFEGLRDAEELQLDPTKIGSFMIRESET 115
 QY 126 RRGYSLSVRLSPASMDIRHRYHICLDNGWLITSPRLTPPSLOALVHYSELADICCC 165
 Db 116 KKGYSLSVR-----HRQVKNHRIEFLRNMYISPRLTFOCLEDLVHYSEVADGLCC 169
 QY 166 LKRCPCVQR-----AGPLRCKDLPPLVYVQRTPLNKKELDSLSEPAATG---EESL 236
 Db 170 VLTPTCLAQNIAPTPSHPSPTGSPGVTLRQKTPDMKRVSRLOEGSEGAENPLVDESL 229
 QY 237 LSEGLRESLFFYISL-NDEAVSLD 259
 Db 230 FSYGLRESIASYLSLTGGDSSSPD 253

RESULT 9
 ID Q13239 PRELIMINARY; PRT; 276 AA.
 AC Q13239;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Putative Src-like adapter protein (SLAP) (SRC-like adapter).
 GN SLAP
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96423054; PubMed=8825655;
 RA Anglist M., Wells D.E., Chakravarti A., Pandey A.;
 RT "Chromosomal localization of the mouse Src-like adapter protein (Slap)
 RT gene and its putative human homolog SLA.";
 RL Genomics 30:623-625(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Meljertink P.H.S., Zorn G., Blikker H., Bolhuis P.A., Baas F.;
 RL Submitted (Feb-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Onusuki T., Hatake K., Ikeda M., Tomizuka H., Terui Y., Uwai M.,
 RA Mura Y.;
 RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
 RA Jonge, Rd, Schlubel M., Wen G., Menzel U., Dettle M., Baumgart C.,
 RA Rosenthal A.;
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BONE MARROW;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: U30473; AAC50357.1; -;
 DR EMBL: U44403; AAC27662.1; -;
 DR EMBL: D89077; BA13758.1; -;
 DR EMBL: AF305872; AAG17933.1; -;
 DR EMBL: BC007042; AAH07042.1; -;
 DR HSSP: P08631; 3HCK.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00019; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR ProDom: PD000093; SH2; 1.

DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR SH3 domain.
 SQ SEQUENCE 276 AA: 31156 MW: 30967CD7B2EAC378 CRC64:
 Query Match 35.98; Score 485.5; DB 4; Length 276;
 Best Local Similarity 40.74; Pred. No. 3e-36;
 Matches 103; Conservative 43; Mismatches 84; Indels 23; Gaps 4;
 QY 9 KSLPSPSSSVQCGQPVTEAEKSKATVAVAGSPAGAPAEELSLRLGSPPLVISEDGW 68
 Db 6 KSTPAPA-----ERLPNPEGIDSDPLAVSDIPSPDISPIIFRGRKLVISDEGW 58
 QY 69 WTVLSEKREYNIPSVAVKSHGWLIGLSREKAEELLPLGNPGAFILRESQTRG 128
 Db 59 WKATSLSTGRESYIPGICVAVYHGMWLFEGLRDAEELQLDPTKIGSFMIRESETRKG 118
 QY 129 SYSLSVRLSPASMDIRHRYHICLDNGWLITSPRLTPPSLOALVHYSELADICCLK 188
 Db 119 FYLSVSR-----HRQVKNHRIEFLRNMYISPRLTFOCLEDLVHYSEVADGLCCVLT 172
 QY 189 EPCVLDQAPRLGKIPPLVYVQRTPLNKKELDSLSEPAATG-----EESLSEGL 241
 Db 173 TPCLTQSTAPAVRASSPVTLRQKTPDMKRVSR---LQDPEGTENPLGVDESILFSYGL 229
 QY 242 RESLFFYISLDE 254
 Db 230 RESIASYLSLTSE 242

RESULT 10
 ID Q9DDK6 PRELIMINARY; PRT; 502 AA.
 AC Q9DDK6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Src-family tyrosine kinase SKC.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protactinopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hordvik I., Male R.;
 RL "A leukocyte cDNA of Atlantic salmon encoding a Src-family tyrosine
 RT kinase.";
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: AF321110; AAG38611.1; -;
 DR HSSP: P08631; 1AD5.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001243; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TYFKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
 DR PROSITE: PS50010; PROTEIN_KINASE_TYR. 1.
 DR PROSITE: PS50001; SH2. 1.
 DR PROSITE: PS50002; SH3. 1.
 KW ATP-binding; Kinase; SH3 domain; Transferase.
 SQ SEQUENCE 502 AA; 56600 MW; 82DF0677AA939900 CRC64;

Query Match 27.4%; Score 370.5; DB 13; Length 502;
 Best Local Similarity 42.4%; Pred. No. 2.2e-25;
 Matches 81; Conservative 29; Mismatches 66; Indels 15; Gaps 3;

QY 15 SLSSVGGCGPYTMEAEKSKATAVALGSPAGPAELSLRLGEPFLTVSEDDGWTYVSE 74
 DB 45 STGSPVSDGP-----ESIAIALYDEGINEDGLGFKKQKXKLIQESGEMVRASI 96
 QY 75 VSGREYIPSVHAKV---HGWLVEGLSREKAEELLIPNPGCAFILRESQTRGSYS 131
 DB 97 STGCEGRIPSNVVAIDSLTEEMFVKGVSKDAEQQLASQNKSGFMIRDEETTKGSGS 156
 QY 132 LSVRLSPASMDIRIRYRHLCDNGMLYISPRFLPSLOALVDHYSLELADICCLLKPPC 191
 DB 157 LSVRDSQSGSDTVKHYKIRTLNDSGYISPRITTTTLQELVSHYKKLDGDLQALVSPC 216

QY 192 VLQRAGPLPGK 202
 DB 217 L----SPKPK 223

RESULT 11

ID 013064 PRELIMINARY; PRT; 488 AA.

AC 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Lyn protein tyrosine kinase.
 GN LYN
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodidae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fukumi Y., Funahiki K., Sato K.;
 RT "Nucleotide sequence of Xenopus lyn protein tyrosine kinase."
 RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
 CC 1. SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: AB003358; BAA20078.1; -;
 DR HSSP: P08631; IAD5.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR Pfam: PF00017; SH2.1.
 DR Pfam: PF00018; SH3.1.
 DR PRINTS: PR00401; SH3DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_Pkinase.1.
 DR ProDom: PD000066; SH3.1.
 DR ProDom: PD000093; SH2.1.
 DR SMART: SM00352; SH2.1.
 DR SMART: SM00356; SH3.1.
 DR SMART: SM00219; TYRK.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS50010; PROTEIN_KINASE_TYR.1.
 DR PROSITE: PS50001; SH2.1.
 DR PROSITE: PS50002; SH3.1.
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 488 AA; 55794 MW; B7E70688BEA92B2 CRC64;

Query Match 27.1%; Score 365.5; DB 13; Length 488;
 Best Local Similarity 38.8%; Pred. No. 6.1e-25;
 Matches 83; Conservative 36; Mismatches 78; Indels 17; Gaps 4;

QY 1 MGLSPSR-----KSLPSPSLSSVGGCGPYTMEAEKSKATAVALGSPAGPAELSL 52
 DB 1 MGLSKSTNPNPDAMGNKNPASTPSLPGQ-KHIDIEGQNVIALPYQGIHEDLS 59
 QY 53 LRLGEPFLTVSEDDGWTYVSEVSGREYIPSVHAKV---SHGWLVEGLSREKAEELL 108
 DB 60 FKKGKELKLEEHGEMWAKSLSTKEGFIENYVAVNTLETSEFFDLTRDAERQ 119
 QY 109 LLAGNGCAFILRESQTRGSYSLSVRLSPASMDIRIRYRHLCDNGMLYISPRFLPS 168
 DB 120 LAGNNPGAFILRESQTRGSYSLSIRDCDPQTDVKKHKIRTLNDSGYISPRITFTS 179
 QY 169 LQALVDHYSLELADICCLLKPCVLRAGPLPGK 202
 DB 180 INEMIOHYOKQADGLCRKLDKPCF---SPKPK 209

RESULT 12

ID 09HB17 PRELIMINARY; PRT; 161 AA.

AC 09HB17;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Src-like adapter protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
 RA Jahn N., Rosenthal A.;
 RT "Chromosome 8 genomic sequence."
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
 CC 1. SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: AF235100; AAC29878.1; -;
 DR HSSP: P08631; 3HCK.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2.1.
 DR Pfam: PF00018; SH3.1.
 DR PRINTS: PR00401; SH3DOMAIN.
 DR ProDom: PD000093; SH2.1.
 DR SMART: SM00252; SH2.1.
 DR SMART: SM00326; SH3.1.
 DR PROSITE: PS50001; SH2.1.
 DR PROSITE: PS50002; SH3.1.
 KW SH3 domain.
 FT NON_TER 161
 SQ SEQUENCE 161 AA; 18493 MW; FC285466804E5B20 CRC64;

Query Match 26.8%; Score 362.5; DB 4; Length 161;
 Best Local Similarity 44.4%; Pred. No. 2.5e-25;
 Matches 75; Conservative 54; Mismatches 54; Indels 13; Gaps 2;

QY 9 KSLPSPSLSSVGGCGPYTMEAEKSKATAVALGSPAGPAELSLRLGEPFLTVSEDDG 68
 DB 6 KSTPAPA-----ERPLPNEGCLSDPLAVLSDVPSDPSPIFFRGKGLVISEDG 58
 QY 69 WTVSEVSGREYIPSVHAKVSHGWLVEGLSREKAEELLIPNPGCAFILRESQTRG 128
 DB 59 WKALSLSTGRESTIPGICVARYHGMLEGLGRDAEELLDPDTKVGSMIRSETTKG 118

OY 129 SYSLSVRLSPASWDRIRHYRICLDNGMLYISPRLTSPSLQALVDHYS 177
 DB 119 FVSLSVR-----HROVKHYRIFRLPNMNYIISPRLTQCLLELDVNHYS 161

RESULT 13

O96INI PRELIMINARY; PRT; 505 AA.
 ID 096INI
 AC 096INI
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Unknown (protein for MGC:16168).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NC NCBITaxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPH;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC007371; AA07371.1;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH2; 1.
 DR ProDom: PD000093; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW ATP-binding; transferase.
 SQ SEQUENCE 505 AA; 57706 MW; B5F739BEF8389176 CRC64;

Query Match

Best Local Similarity 26.4%; Score 356.5; DB 4; Length 505;
 Matches 76; Conservative 24; Mismatches 67; Indels 5; Gaps 2;

OY 25 PVTMEARSKATNALGSPAGPAELSLRLGEPLTVSEDDQMTVLSEVSGREVNIPS 84
 DB 51 PDEHLDDEKHFVVALDYAMNDRDLQMLGKELQVKGTDMMWLARSILVYTGREGYVPS 110
 OY 85 VHVAVS---HGMLEYGLSRKAEELLLPGNPGGAFILRESOTRRGSSLSVRSRA 140
 DB 111 NFVARVESLEMERWFFRSGCRKEARQLAPINKAGSFLIRSEETNKAGSLSVK-DVTT 169
 OY 141 SMDRIHRIHICLDNGMLYISPRLTSPSLQALVDHYSLEADICCLKEPCV 192
 DB 170 QGELIKHKIKICLDGEGYISPRITFPSLQALVQHSKKGDLGCLRLTLPCV 221

RESULT 14

O95M32 PRELIMINARY; PRT; 509 AA.
 ID 095M32
 AC 095M32
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Lck protein.
 CN LCK.
 OS Hylobates sp. (gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 NC NCBITaxid=9581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pizard C.;

RL Thesis (2001), Department of Experimental Oncology Laboratory, U.
 DR EMBL: AJ320182; CAC44027.1;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50019; PROTEIN_KINASE_TYR; UNKNOWN_1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW ATP-binding; transferase.
 SQ SEQUENCE 509 AA; 57946 MW; F1BF5C237C8D87E CRC64;

Query Match 25.5%; Score 344; DB 6; Length 509;
 Best Local Similarity 41.1%; Pred. No. 6e-23;
 Matches 74; Conservative 26; Mismatches 70; Indels 10; Gaps 2;

OY 26 VTMERASKAT-----AVAGSPFAGPAELSLRLGEPLTVSEDDQMTVLSEVSGRE 79
 DB 49 VTTEGSNPASPLODNLVIALHSYEPSHDGLGEKEGEOURLIEGSEGMKAQSLTTGCE 108
 OY 80 YNIPSVHAKVS---HGMLEYGLSRKAEELLLPGNPGGAFILRESOTRRGSSLSVRS 135
 DB 109 GFIPFNVAKANSLPEPEWFKNLSSKAEQRLAPRNTGSLIRSEETNKAGSLSVRS 168
 OY 136 LSPASWDRIRHYRICLDNGMLYISPRLTSPSLQALVDHYSLEADICCLKEPCV 195
 DB 169 DFGONGGEVVKHYRIKRLNDNGGFTISPRITFGLHVLRYHNASDGLCTRSLSPCOTK 228

RESULT 15

O91X65 PRELIMINARY; PRT; 509 AA.
 ID 091X65
 AC 091X65
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Similar to lymphocyte-specific protein tyrosine kinase.
 CN LCK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBITaxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPINALVARY GLAND;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC011474; AA11474.1;
 DR WGD: MG1:96756; LCK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50019; PROTEIN_KINASE_TYR; UNKNOWN_1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW ATP-binding; kinase; transferase.

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SO SEQUENCE 509 AA: 57942 MW: 3513102F49A7FDOB CRC64:

Query Match 25.4%; Score 342.5; DB 11; Length 509;
Best Local Similarity 39.6%; Pred. No. 8.2e-23;

Matches 78; Conservative 28; Mismatches 84; Indels 7; Gaps 2;

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QY 3 SLPSRRKSLPSPSLSSVGGGPPVTMEAEKSKATAVALGSPFAGGPAELSLRLGEPLTV 62
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 35 SLPIINGSEVNDPL--VTEGSLPPASPLQDNLYIALHSTPEPSHDGDLGFEKGEOLRIL 91
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 63 SEDGDMWTVLSEVSGREYNIPSYHAKYS---HGMVTEGLSREKAEELLILPGNPGAF 118
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 92 EDSGEWKAOSLTGTGEGFIPFNFAKANSLEPEPWFKNLSRKDAEROLLAPONTGSEF 151
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 119 LIPESQTRRGSYSLSVRLSRPASWDRIHRIHCLDNGWLYISPRITPPSLQALVDHYSE 178
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 152 LIPESSTAGSPSLSVDFDONGEVVKKIRNLNDNGCFYISPRITPPGLHDLVRRHYTN 211
   : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 179 LADDICLLKEPCVLQR 195
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 212 ASDGICTKLSRPCQOTK 228
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: March 24, 2003, 15:50:32
Job time : 46.8955 secs